

1/9

## DD4b5.3 Coding Sequence

Length 2563 bp

GGCGCGGGCAGGTCGGAGCTCGGAGCTGCTGCTTCTGGTTCTCTTGTGGCCACCGTCGCT  
1 -----+-----+-----+-----+-----+ 60  
R G Q V G A R S C C F W F S C G H R R C -

GTCCGGCTGCCTTGGGCTGCCGAACAGACAAGGCGTGGGCCACAGCACCTCAGAAGCCGA  
61 -----+-----+-----+-----+-----+ 120  
P A A L G C R T D K A W A T A P Q K P T -

CGCAGCTCGACGCAGGGGCGGCAGGAGGGTGGGCGATCGCGTGTCTGGAGGGCGCCGCGC  
121 -----+-----+-----+-----+-----+ 180  
Q L D A G A G R R V G D R V S E G A A R -

GGGCAGGCGGGCGGGCGCCAGAGGGGAAAGAGGCGGGGGCGGCGGGTCAAGCGCTGGCC  
181 -----+-----+-----+-----+-----+ 240  
A G G R A P E G E R G G G G G S A A G R -

GGGCCGGCGGGGGAATGTCGATGCCTGACGCGATGCCGCTGCCCGGGGTCGGGGAGGAGC  
241 -----+-----+-----+-----+-----+ 300  
A G G G M S M P D A M P L P G V G E E L -

TGAAGCAGGCCAAGGAGATCGAGGACGCCGAGAAGTACTCCTTCATGGCCACCGTCACCA  
301 -----+-----+-----+-----+-----+ 360  
K Q A K E I E D A E K Y S F M A T V T K -

AGGCGCCCAAGAAGCAAATCCAGTTTGCTGATGACATGCAGGAGTTCACCAAATTCCTCA  
361 -----+-----+-----+-----+-----+ 420  
A P K K Q I Q F A D D M Q E F T K F P T -

CCAAACTGGCCGAAGATCTTTGTCTCGCTCGATCTCACAGTCTTCCACTGACAGCTACA  
421 -----+-----+-----+-----+-----+ 480  
K T G R R S L S R S I S Q S S T D S Y S -

GTTTCAGCTGCATCCTACACAGATAGCTCTGATGATGAGGTTTCTCCCGAGAGAAGCAGC  
481 -----+-----+-----+-----+-----+ 540  
S A A S Y T D S S D D E V S P R E K Q Q -

AAACCAACTCCAAGGGCAGCAGCAATTTCTGTGTGAAGAACATCAAGCAGGCAGAATTTG  
541 -----+-----+-----+-----+-----+ 600  
T N S K G S S N F C V K N I K Q A E F G -

GACGCCGGGAGATTGAGATTGCAGAGCAAGACATGTCTGCTCTGATTTCACTCAGGAAAC  
601 -----+-----+-----+-----+-----+ 660  
R R E I E I A E Q D M S A L I S L R K R -

GTGCTCAGGGGAGAAGCCCTTGGCTGGTGCTAAATAGTGGGCTGTACACACATCACAG  
661 -----+-----+-----+-----+-----+ 720  
A Q G E K P L A G A K I V G C T H I T A -

CCCAGACAGCGGTGTTGATTGAGACACTCTGTGCCCTGGGGGCTCAGTGCCGCTGGTCTG  
721 -----+-----+-----+-----+-----+ 780  
Q T A V L I E T L C A L G A Q C R W S A -

CTTGTAACATCTACTCAACTCAGAATGAAGTAGCTGCAGCACTGGCTGAGGCTGGAGTTG  
781 -----+-----+-----+-----+-----+ 840  
C N I Y S T Q N E V A A A L A E A G V A -

CAGTGTTCGCTTGGAAGGGCGAGTCAGAAGATGACTTCTGGTGGTGTATTGACCGCTGTG  
841 -----+-----+-----+-----+-----+ 900  
V F A W K G E S E D D F W W C I D R C V -

TGAACATGGATGGGTGGCAGGCCAACATGATCCTGGATGATGGGGGAGACTTAACCCACT  
901 -----+-----+-----+-----+-----+ 960  
N M D G W Q A N M I L D D G G D L T H W -

FIG. 1

2/9

GGGTTTATAAGAAGTATCCAAACGTGTTTAAGAAGATCCGAGGCATTGTGGAAGAGAGCG  
961 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1020  
V Y K K Y P N V F K K I R G I V E E S V -

TGACTGGTGTTCACAGGCTGTATCAGCTCTCCAAAGCTGGGAAGCTCTGTGTTCCGGCCA  
1021 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1080  
T G V H R L Y Q L S K A G K L C V P A M -

TGAACGTCAATGATTCTGTTACCAAACAGAAGTTTGATAACTTGTAAGTCTGCTGCCGAGAAT  
1081 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1140  
N V N D S V T K Q K F D N L Y C C R E S -

CCATTTTGGATGGCCTGAAGAGGACCACAGATGTGATGTTTGGTGGGAAACAAGTGGTGG  
1141 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1200  
I L D G L K R T T D V M F G G K Q V V V -

TGTGTGGCTATGGTGAGGTAGGCAAGGGCTGCTGTGCTGCTCTCAAAGCTCTTGGAGCAA  
1201 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1260  
C G Y G E V G K G C C A A L K A L G A I -

TTGTCTACATTACCGAAATCGACCCCATCTGTGCTCTGCAGGCCTGCATGGATGGGTTCA  
1261 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1320  
V Y I T E I D P I C A L Q A C M D G F R -

GGGTGGTAAAGCTAAATGAAGTCATCCGGCAAGTCGATGTCGTAATAACTTGCACAGGAA  
1321 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1380  
V V K L N E V I R Q V D V V I T C T G N -

ATAAGAATGTAGTGACACGGGAGCACTTGGATCGCATGAAAAACAGTTGTATCGTATGCA  
1381 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1440  
K N V V T R E H L D R M K N S C I V C N -

ATATGGGCCACTCCAACACAGAAATCGATGTGACCAGCCTCCGCACTCCGGAGCTGACGT  
1441 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1500  
M G H S N T E I D V T S L R T P E L T W -

GGGAGCGAGTACGTTCTCAGGTGGACCATGTCATCTGGCCAGATGGCAAACGAGTTGTCC  
1501 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1560  
E R V R S Q V D H V I W P D G K R V V L -

TCCTGGCAGAGGGTCGTCTACTCAATTTGAGCTGCTCCACAGTTCCACCTTTGTTCTGT  
1561 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1620  
L A E G R L L N L S C S T V P T F V L S -

CCATCACAGCCACAACACAGGCTTTGGCACTGATAGAACTCTATAATGCACCCGAGGGGC  
1621 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1680  
I T A T T Q A L A L I E L Y N A P E G R -

GATACAAGCAGGATGTGTACTTGCTTCCTAAGAAAATGGATGAATACGTTGCCAGCTTGC  
1681 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1740  
Y K Q D V Y L L P K K M D E Y V A S L H -

ATCTGCCATCATTTGATGCCACCTTACAGAGCTGACAGATGACCAAGCAAAATATCTGG  
1741 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1800  
L P S F D A H L T E L T D D Q A K Y L G -

GA CTCAACAAAAATGGGCCATTCAAACCTAATTATTACAGATACTAATGGACCATACTAC  
1801 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1860  
L N K N G P F K P N Y Y R Y \*

CAAGGACCAGTCCACCTGAACCACACACTCTAAAGAAATATTTTTTAAGATAACTTTTAT  
1861 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1920

TTTCTTCTTACTCCTTTCTGTTGATTTTTTCTCTATAATTCATTCTTGTTTTTTCATC  
1921 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1980

TCATTATCCAAGTTCTGCAGACCACACAGGAAGTTGCTTCATGGCTCTTTAGATGAAATA  
1981 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 2040

FIG 1 (cont)

3/9

2041 GAAGTTCAGGGTCCCTCACTCTAGTCACTAAAGAAGGATTTTACTCCCCCAGCCCAGAAA 2100  
-----+-----+-----+-----+-----+-----+  
2101 GGTGATTCTTCTCTTTACCATTTCTGGGGACTTTAGTCTTAATTAGGTACCTTATTAACA 2160  
-----+-----+-----+-----+-----+-----+  
2161 GGAAATGCTAAGGTACCTTCTCTGTGGAACAATCTGCAATGTCTAAATCGCCTTAAAAGA 2220  
-----+-----+-----+-----+-----+-----+  
2221 GCCCATTTCTTAGCTGCTGAAATCAGTGCTCTTTCACCTTCTTCAGAGAAGCAGGGATGGT 2280  
-----+-----+-----+-----+-----+-----+  
2281 ACCTACCCGGCAGGTAGGTTAGATGTGGGTGGTGCATGTTAATTTCCCTTAGAAGTTCCA 2340  
-----+-----+-----+-----+-----+-----+  
2341 AGCCCTGTTTCCTGCGTAAAGGTGGTATGTCCAGTTCAGAGATGTGTATAATGAGCATGG 2400  
-----+-----+-----+-----+-----+-----+  
2401 CTTGTTAAGATCAGGAGGCCCACTTGGATTTATAGTATAGCCCTTCCTCCACTCCCACCA 2460  
-----+-----+-----+-----+-----+-----+  
2461 GACTTGCTCATTTTTTCGAGTTTTTAACTAGACTACACTCTATTTGAGTTTAATTTTGTCC 2520  
-----+-----+-----+-----+-----+-----+  
2521 TCTAGGATTTATTTCTGTTGTCCAAAAAAAAAAAAAAAAAAAAA 2563  
-----+-----+-----+-----+-----+-----+

FIG 1 (Cont)

For sequence

Alignment of DD4b5.3 AHCY-like domain with full-length AHCY amino acid sequences of human (hu), mouse (mu) and drosophila (dr).  
Noted are conserved features shown to be important for AHCY function.



FIG 2

DD4b5.3 sequenc sch matic

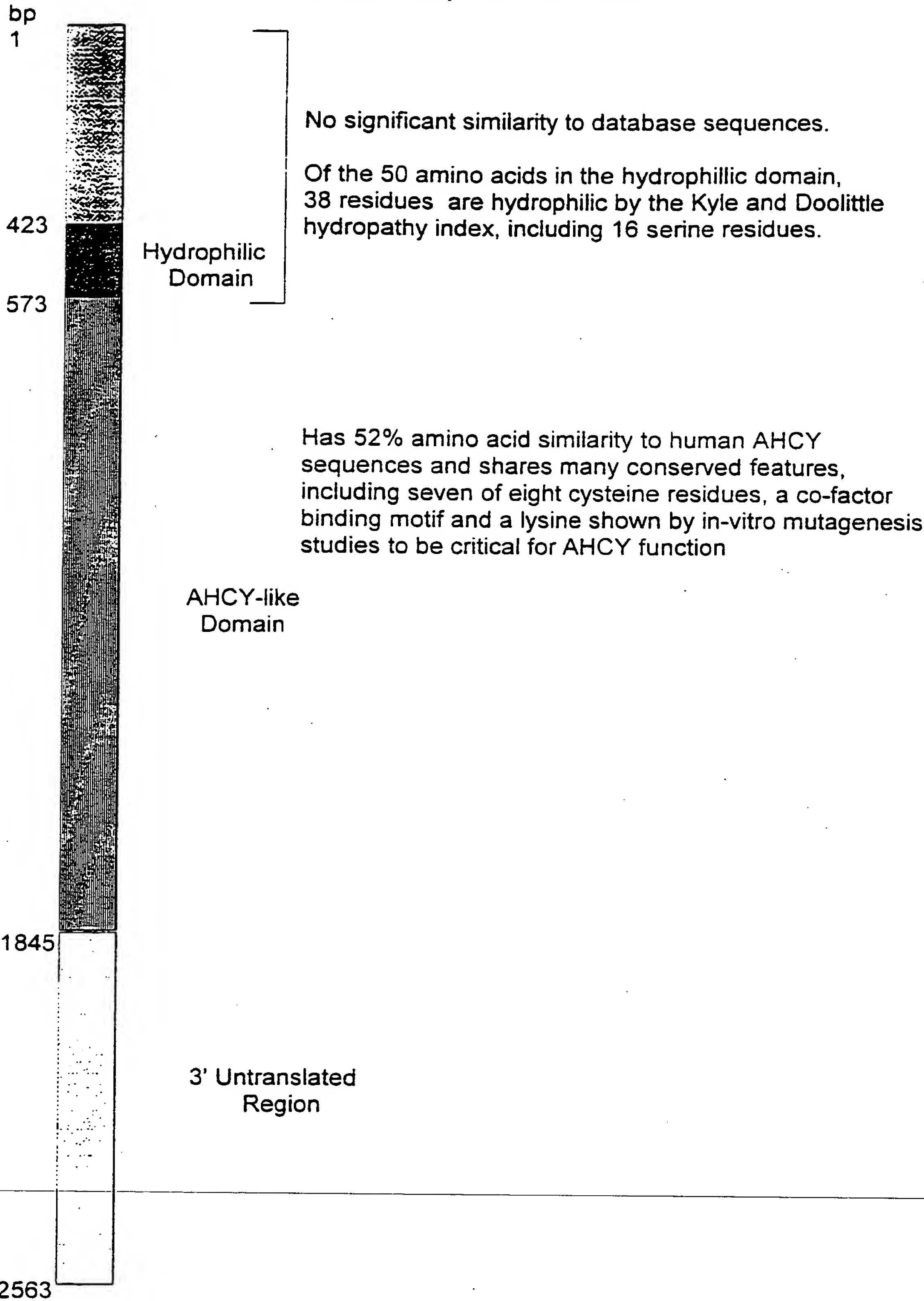
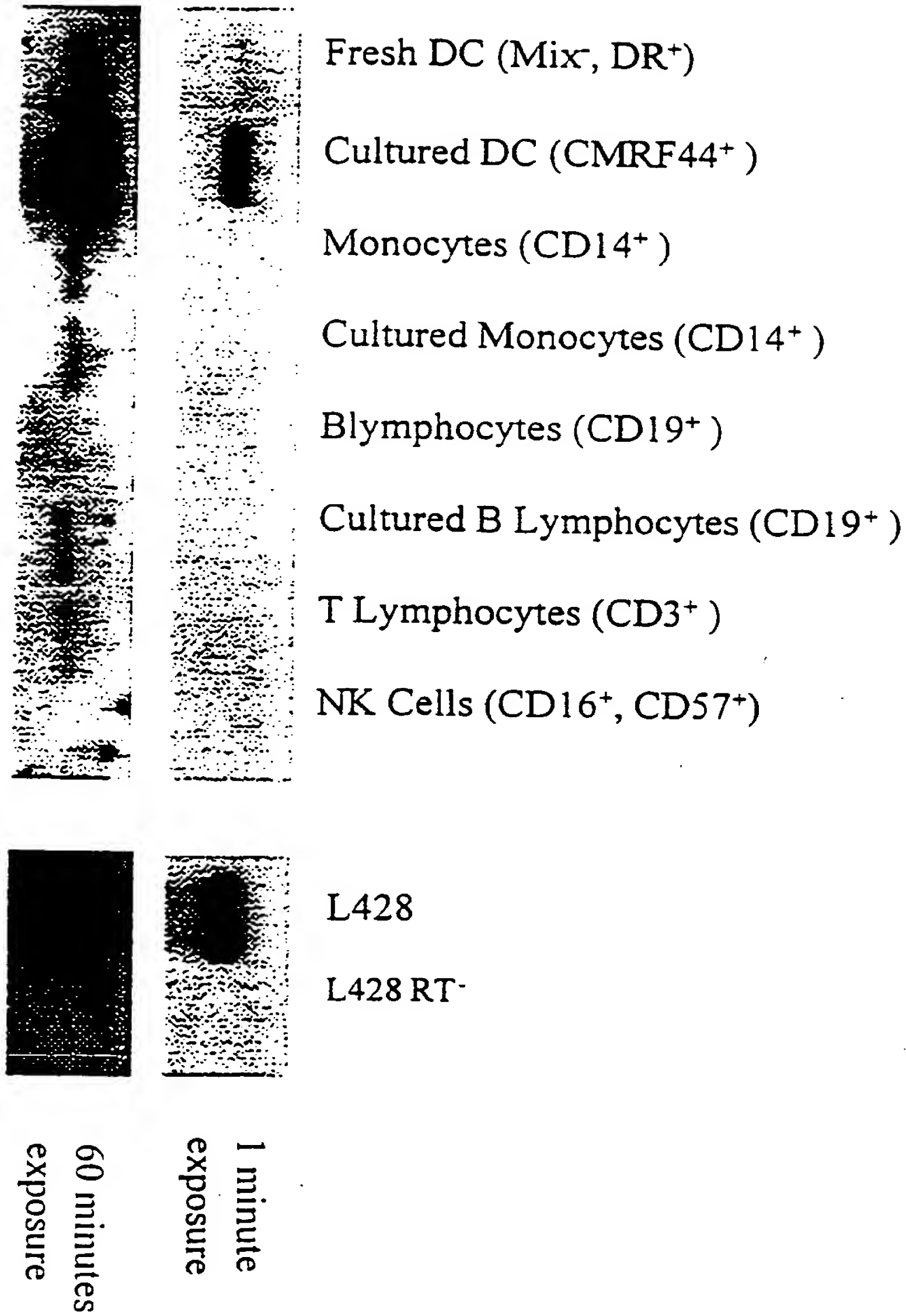


FIG 3

09703091-0001401



Southern blot analysis of DD4b5.3 RT-PCR results

FIG 4



Expression of DD4b5.3 in DC lineage panel, as assessed by RT-PCR

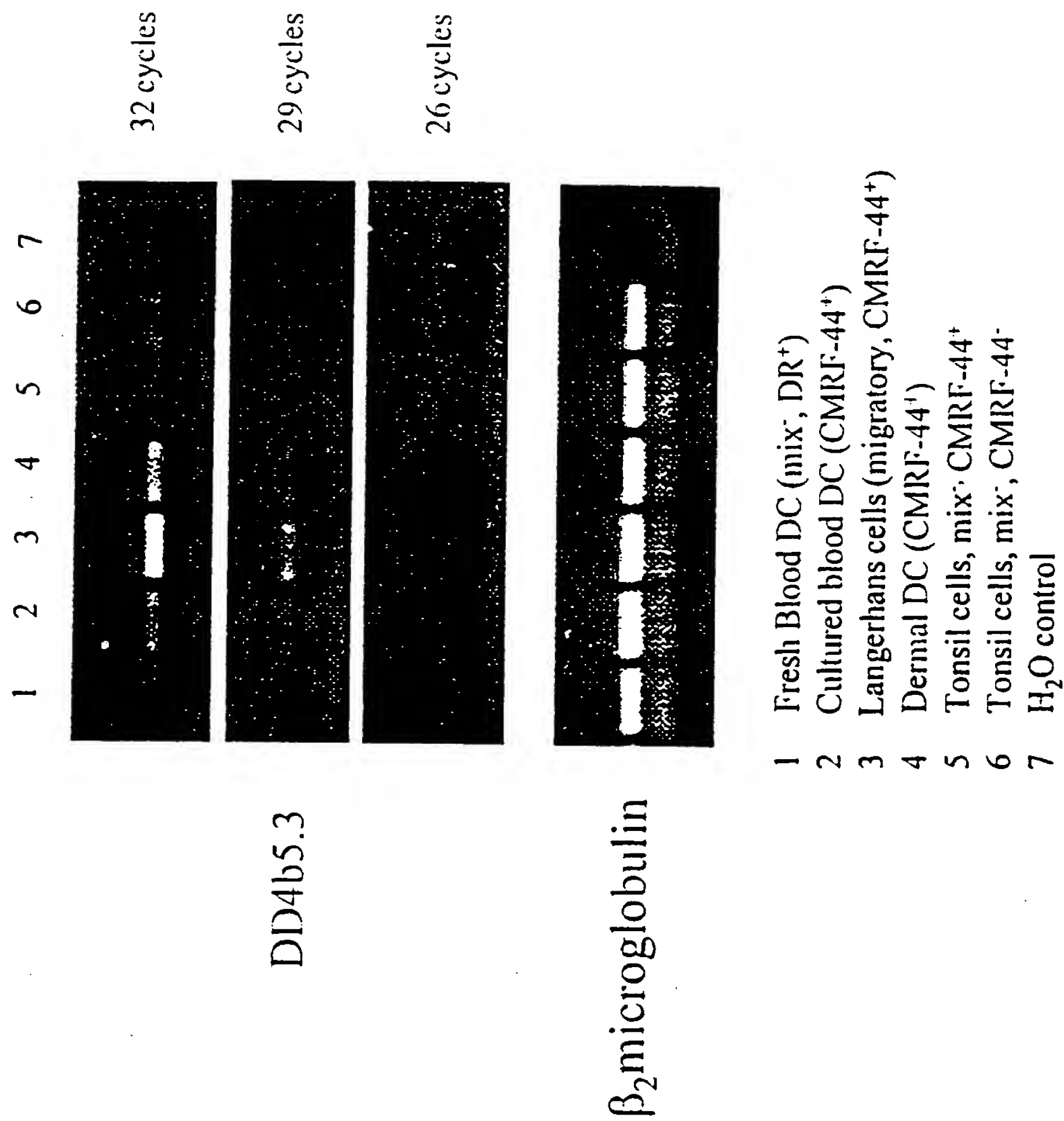


FIG 5



**THE**      **WORLD'S**      **LARGEST**



# RAP-PCR Method

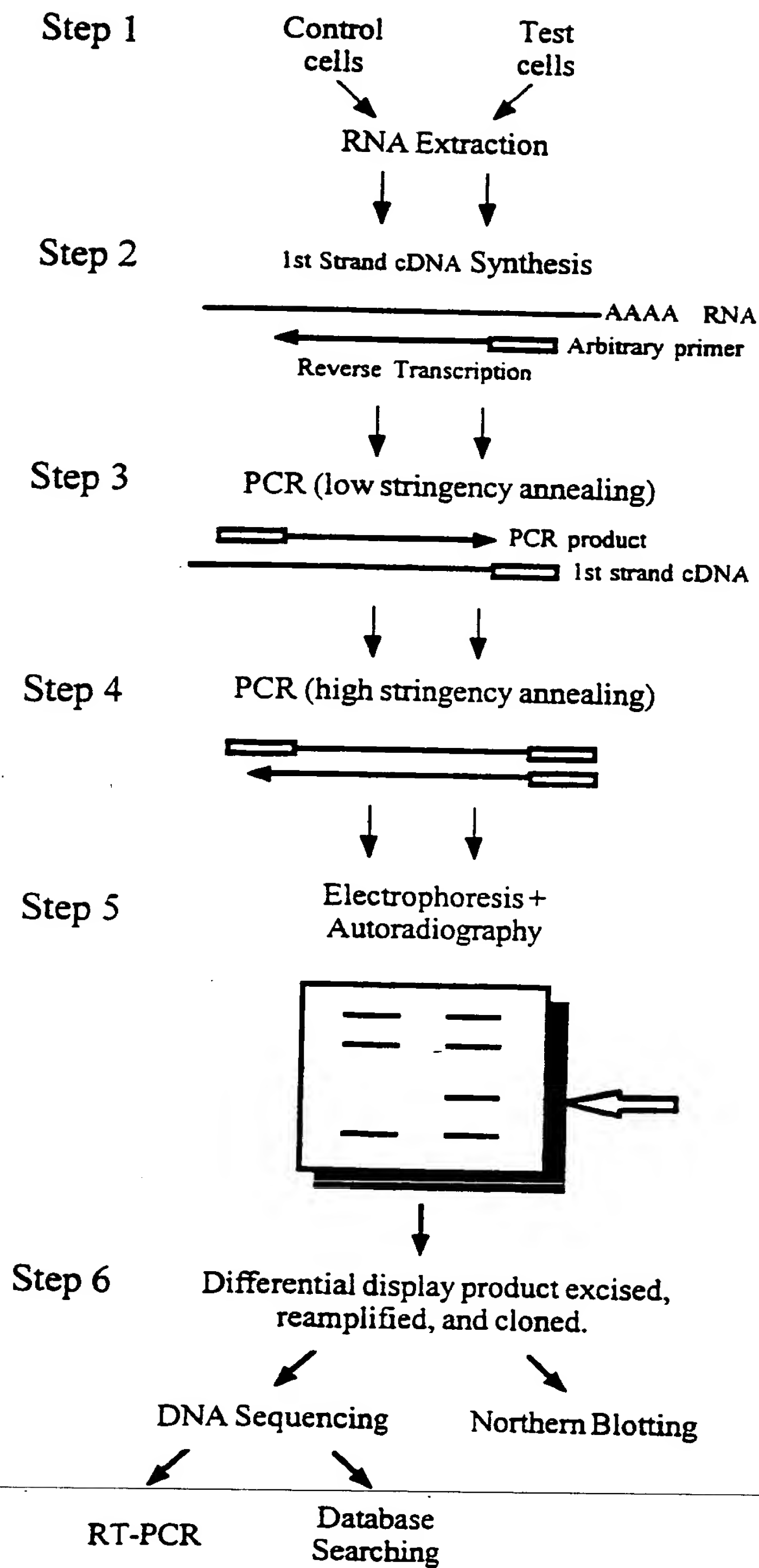


FIG 7